#17

Interview Summary

Application No.	Applicant(s)	
09/325,603	Svendsen et al.	
Examiner	Group Art Unit	
Elizabeth Slobodyansky	1652	

All participants (applicant, applicant's representative, PTO personnel):

(1) *Elizabeth Slobodyansky* (3) *Jason Garbell*

(2) *Nashaat Nashed* (4) *Sten Knudsen (5) Anne-Marie H. Jorsboe*

Date of Interview *Feb 14, 2001*

Type: ☐ Telephonic ☒ Personal (copy is given to ☐ applicant ☒ applicant's representative).

Exhibit shown or demonstration conducted: ☐ Yes ☒ No. If yes, brief description:

Agreement ☐ was reached. ☒ was not reached.

Claim(s) discussed: *all of record*

Identification of prior art discussed:

Description of the general nature of what was agreed to if an agreement was reached, or any other comments:
The way to claim the subject matter has been discussed. Applicant has been adviced that the claim method should consider a step of modelling a structure of a parent amylase on the crystal structure of SEQ ID NO:13 defined by the coordinates depicted in Appendix.

(A fuller description, if necessary, and a copy of the amendments, if available, which the examiner agreed would render the claims allowable must be attached. Also, where no copy of the amendents which would render the claims allowable is available, a summary thereof must be attached.)

1. ☒ It is not necessary for applicant to provide a separate record of the substance of the interview.

Unless the paragraph above has been checked to indicate to the contrary, A FORMAL WRITTEN RESPONSE TO THE LAST OFFICE ACTION IS NOT WAIVED AND MUST INCLUDE THE SUBSTANCE OF THE INTERVIEW. (See MPEP Section 713.04). If a response to the last Office action has already been filed, APPLICANT IS GIVEN ONE MONTH FROM THIS INTERVIEW DATE TO FILE A STATEMENT OF THE SUBSTANCE OF THE INTERVIEW.

2. ☐ Since the Examiner's interview summary above (including any attachments) reflects a complete response to each of the objections, rejections and requirements that may be present in the last Office action, and since the claims are now allowable, this completed form is considered to fulfill the response requirements of the last Office action. Applicant is not relieved from providing a separate record of the interview unless box 1 above is also checked.

E. Slobodyansky

ELIZABETH SLOBODYANSKY
PRIMARY EXAMINER
ART UNIT 1652

Examiner Note: You must sign and stamp this form unless it is an attachment to a signed Office action.

Telefax

novozymes®

No. of pages incl. this:

Telefax no.: 703-308-~~3809~~ 4242

[redacted]

Date: 2/13/01

To: Examiner Slobodyansky

cc:

From: Jason I. Garbell, Esq.

Message:

Please Hand Deliver to the Examiner today

Novozymes North America, Inc.
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Att.: Examiner
Slobodyansky

13 February 2001
KOPa

USSN # 09/325,603

Dear Examiner Slobodyansky:

Enclosed please find (3) pages of proposed new claims in the above referenced case. The claims are intended for discussion purposes only.

Best Regards,

Kelley O'Patry
Assistant to Jason I. Garbell, Esquire

Novozymes A/S

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FOR DISCUSSION PURPOSES ONLY

PROPOSED NEW CLAIMS FOR SERIAL NO. 09/325,603

79. A method of producing a variant of a parent alpha-amylase having an altered property relative to said parent alpha-amylase, wherein said parent alpha-amylase has a sequence at least 70% homologous to the sequence of SEQ ID Nos: ~~2, 4, 6~~ and 13, when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, said method comprising:

(a) providing a three-dimensional alpha-amylase structure; wherein said three-dimensional alpha-amylase structure has an A domain, a B domain and a C domain, wherein said A domain has an amino acid sequence corresponding to residues 1-103 and 206-395 of SEQ ID NO: 2 and a three-dimensional structure represented by the corresponding amino acid coordinates of SEQ ID NO. 13 depicted in Appendix 1; said B domain has an amino acid sequence corresponding to residues 104-205 of SEQ ID NO:2 and a three-dimensional structure represented by the corresponding amino acid coordinates of SEQ ID NO.13 depicted in Appendix 1; and said C domain has an amino acid sequence corresponding to residues 396-483 of SEQ ID NO:2 and having a three-dimensional structure represented by the corresponding amino acid coordinates of SEQ ID NO.13 depicted in Appendix 1;

(b) identifying in said three-dimensional alpha-amylase structure provided in said (a) at least one amino acid residue or at least one structural part; wherein an alteration in said at least one amino acid residue or said at least one structural part is predicted to result in an altered property, and wherein said altered property is selected from the group consisting of substrate specificity, substrate binding, substrate cleavage pattern, temperature stability, pH dependence of enzymatic activity, pH dependence of stability, stability towards oxidation, Ca^{2+}-dependency and specific activity;

(c) translating said at least one amino acid residue or at least one structural part identified in said (b) into a corresponding at least one amino acid residue or at least one structural part in said parent alpha-amylase;

(d) modifying the sequence of a nucleic acid encoding said parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said at least one amino acid residue or at least one structural part identified in said (b); and

(e) expressing the modified nucleic acid in a host cell to produce said variant alpha-amylase, wherein said variant has alpha-amylase enzymatic activity and has at least one altered property relative to said parent alpha-amylase.

80. A method of producing a variant of a parent alpha-amylase having an altered property relative to said parent alpha-amylase, wherein said parent alpha-amylase has a sequence at least 70% homologous to the sequence of SEQ ID Nos: 2, 4, 6 and 13 when homology is determined by the GAP program (Genetic Computer Group, Version 7.0) using default values for GAP penalties, said method comprising:

(a) providing a three-dimensional alpha-amylase structure of said parent alpha-amylase; wherein said three-dimensional alpha-amylase structure has an A domain, a B domain and a C domain, wherein said A domain has an amino acid sequence corresponding to residues 1-103 and 206-395 of SEQ ID NO: 2 and a three-dimensional structure represented by the corresponding amino acid coordinates of SEQ ID NO. 13 depicted in Appendix 1; said B domain has an amino acid sequence corresponding to residues 104-205 of SEQ ID NO:2 and a three-dimensional structure represented by the corresponding amino acid coordinates of SEQ ID NO.13 depicted in Appendix 1; and said C domain has an amino acid sequence corresponding to residues 396-483 of SEQ ID NO:2 and having a three-dimensional structure represented

by the corresponding amino acid coordinates of SEQ ID NO.13 depicted in Appendix 1;

(b) identifying in said three-dimensional structure provided in said (a) at least one amino acid residue or at least one structural part; wherein an alteration in said at least one amino acid residue or said at least one structural part is predicted to result in an altered property, and wherein said altered property is selected from the group consisting of substrate specificity, substrate binding, substrate cleavage pattern, temperature stability, pH dependence of enzymatic activity, pH dependence of stability, stability towards oxidation, Ca^{2+}-dependency and specific activity;

(c) modifying the sequence of a nucleic acid encoding said parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said at least one amino acid residue or at least one structural part identified in said (b); and

(d) expressing the modified nucleic acid in a host cell to produce said variant alpha-amylase, wherein said variant has alpha-amylase enzymatic activity and has at least one altered property relative to said parent alpha-amylase.